

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

sequence listing S-92981.ST25
SEQUENCE LISTING

<110> Durfee, Tim
Feiler, Heidi
Gruissem, Wilhelm
Jenkins, Susan
Roe, Judith
Zambryski, Patricia

<120> Alteration of Plant Meristem Function by Manipulation of the Retinoblastoma-Like Plant RRB Gene

<130> S-92981

<140> US 09/527,084

<141> 2000-03-16

<150> US 60/125,229

<151> 1999-03-19

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 3474

<212> DNA

<213> Arabidopsis Thaliana

```

<400> 1
gaagtcaggt gaagatagag agagacactg agaggaggga aaatttgtag ggttttcgga      60
gatctctgtg attcctctga atttgctgaa ttttttcgag gaggcgtag aagtcgggct      120
tcttaaaaaat cagatcttct gctcaggctt taatcggcga cgtctggtat tgggatctgt      180
gacacaaaaa gctgcgttgg agactatgga agaagttcag cctccagtga ccccgcccat      240
tgaaccaaat gggaaaagaa gcgaagcctc tctcttggaac atatgcgaga aagttctgtc      300
tcttgatggg agcacttgcg atgaagcttt gaagttgttt acagaaacca aacgaatttt      360
gtcagcaagc atgtctaaca ttggaagtgg aacgcgggaa gaagtagaga ggttctggtt      420
tgcggtttatt ctctattcag tgaagaggct tagtgtgaga aaagaagcgg atggtctgtc      480
agtgtctggt gataatgagt ttaatctatg tcagatactg agggctctga agctaaatat      540
tgtggatttt tttaaagagt tacctcagtt tgtggtcaag gctggatctg tactgggtga      600
actttacggc gcagactggg agaacagact tcaggcaaag gaggtgcagg ctaactttgt      660
gcatcttagc cttctaagca aatactacaa acgtgggttc cgggaattct ttttgacata      720
tgatgcaaac gcagaaaaga actcagcaaa ctcttctacc tatttgctgg atagttatcg      780
ttttgatggg ctactctttt tggcactccg aaaccatgcg tttagtcgat ttaaggacct      840
cgtgacatgc tcaaatggcg tagtttctat attggctatt ttgatcatac atgttcottg      900

```

sequence listing S-92981.ST25

tcggtttaga aatttcagca tccaagattc ttctcgcttt gttaagaaag gtgacaaagg	960
tgtagacttg gttgcatcac ttgcaagat atatgacgcc tcagaagatg agttgaggat	1020
agtaattgac aaggcaaata atttggtaga aaccatactg aagaaaaagc catctccagc	1080
atctgagtgc caaactgaca agctagataa tattgacca gatggcttga cctactttga	1140
ggatttactg gaagagacgt ccatctcaac tagcttaatt acacttgaaa aggattacta	1200
tgatggtaaa ggcgaacttg atgagagggt attcatcaat gaagaggata gcttacttgg	1260
atctggaagc ttatctgcag gagctgttaa tattactggg gttaagagga aaattgatgc	1320
tttgagctca cctgcaagga catttataag cccactttct cctcataagt cgcttgcgc	1380
taagacaaat ggtattagcg gtgctaccaa gttggcagca acaccagtga gcacagcaat	1440
gacaactgcc aagtggctca ggactgtcat atccccgctt ctgccaaaac cttctcctgg	1500
gttggaacat ttccttaaat catgtgatag ggatataaca aatgacgtca cacgaagagc	1560
acacataata ttggaagcta ttttccaaa tagttccctt ggtgcccaat gtggagggtg	1620
aagtttgcaa gctgttgacc tgatggatga catatgggca gagcagcgca gattagaagc	1680
ttgtaagtta tactacagag ttcttgaggc aatgtgtaaa gcagaagctc agattttgca	1740
tgcaaataat ctgaactctt tattgacaaa tgagagggtc catagatgca tgcttgcttg	1800
ctcagctgaa ttggtactgg ctaccacaaa aacaattaca atgttggtcc cagctgttct	1860
ggagaggact gggatcacag cctttgatct cagcaaggta attgagagtt tcatacgaca	1920
tgaagattct ctgcctagag agttgagacg acatctgaat tcaactggagg aacggcttct	1980
agagagtatg gtatgggaga aaggctcttc aatgtacaat tctctgattg ttgccaggcc	2040
atcgcttgca ttggagataa atcagctcgg ttactagct gaaccaatgc catctctgga	2100
tgcaatcgca gcacttatta atttctctga cggagcaaat catgcatcat ctgtacaaaa	2160
gcatgaaact tgtccaggac aaaatggggg gattagatcg cccaaaagat tatgtactga	2220
ttaccgcagc attctagttg aacgcaattc ctttacatca ccagtaaagg atcgtctgtt	2280
ggccttaggc aacgttaaat ccaagatgct gccacctccg ttgcagtctg catttgccag	2340
cccaacacgg cccaaccag gaggtggagg agaaacttgt gcagaaactg gaatcaatat	2400
tttcttcaca aagattaata aattggctgc tgtaagaatc aatggaatgg tggaagact	2460
acaactttca cagcaaataa gggagagtgt gtattgtttc ttccaacatg tacttgctca	2520
gcggacttct cttttattca gtcgacacat tgaccagatc attctctgtt gcttctacgg	2580
agtggccaag atatcccaaa tgagcctgac tttcagggaa atcatatata actaccggaa	2640

sequence listing S-92981.ST25

gcaaccacag tgtaaaccat tagttttccg cagcgtttat gtggatgcgt tacaatgtcg 2700
 ccgtcaaggg agaatagggc cagatcatgt tgacatcatc acattctaca atgaaatatt 2760
 tattcctgcc gtaaagccgc tgctgggtgga gctaggtcct gtaagaaacg accgggctgt 2820
 ggaagccaat aataagcctg aagggtcaatg tcccggatcg ccaaaggtgt ctgtgtttcc 2880
 aagtgttcca gacatgtccc ctaaaaaagt atctgcagtg cacaatgttt atgtttctcc 2940
 tcttcgggga tcaaagatgg atgctcttat ttcacacagt acaaagagtt actatgcttg 3000
 tgttggagag agtacacatg cttaccagag cccttcaaag gacctatctg ccatcaacaa 3060
 ccgcttgaac aacagcagca gcaaccgcaa gaggacgcta aactttgacg cagaagcagg 3120
 gatggtcagc gattccatgg tagcaaatag ccttaacctc caaaaccaa atcaaaacca 3180
 aaatggaagc gatgcatcgt cctcaggtgg tgccgcaccc cttaaaaccg agccaacaga 3240
 ttcatagata tctctctcta cttgctacac caacttctct tcagttatag catctgtaaa 3300
 tccttatgtt gcagagtttg cttttatgtt tagctttcta gtttatagtg atcacctcag 3360
 gctatgagcg gatggatccc tttattgttt cttttttctt tttttatctt agttaagtca 3420
 gtcttaataa gcattaataa atgtcttttt cttgttcaaa aaaaaaaaaa aaaa 3474

<210> 2
 <211> 1013
 <212> PRT
 <213> Arabidopsis Thaliana

<400> 2

Met Glu Glu Val Gln Pro Pro Val Thr Pro Pro Ile Glu Pro Asn Gly
 1 5 10 15
 Lys Arg Ser Glu Ala Ser Leu Leu Asp Ile Cys Glu Lys Val Leu Ser
 20 25 30
 Leu Asp Gly Ser Thr Cys Asp Glu Ala Leu Lys Leu Phe Thr Glu Thr
 35 40 45
 Lys Arg Ile Leu Ser Ala Ser Met Ser Asn Ile Gly Ser Gly Thr Arg
 50 55 60
 Glu Glu Val Glu Arg Phe Trp Phe Ala Phe Ile Leu Tyr Ser Val Lys
 65 70 75 80
 Arg Leu Ser Val Arg Lys Glu Ala Asp Gly Leu Ser Val Ser Gly Asp
 85 90 95

sequence listing S-92981.ST25

Asn Glu Phe Asn Leu Cys Gln Ile Leu Arg Ala Leu Lys Leu Asn Ile
100 105 110

Val Asp Phe Phe Lys Glu Leu Pro Gln Phe Val Val Lys Ala Gly Ser
115 120 125

Val Leu Gly Glu Leu Tyr Gly Ala Asp Trp Glu Asn Arg Leu Gln Ala
130 135 140

Lys Glu Val Gln Ala Asn Phe Val His Leu Ser Leu Leu Ser Lys Tyr
145 150 155 160

Tyr Lys Arg Gly Phe Arg Glu Phe Phe Leu Thr Tyr Asp Ala Asn Ala
165 170 175

Glu Lys Asn Ser Ala Asn Ser Ser Thr Tyr Leu Leu Asp Ser Tyr Arg
180 185 190

Phe Gly Trp Leu Leu Phe Leu Ala Leu Arg Asn His Ala Phe Ser Arg
195 200 205

Phe Lys Asp Leu Val Thr Cys Ser Asn Gly Val Val Ser Ile Leu Ala
210 215 220

Ile Leu Ile Ile His Val Pro Cys Arg Phe Arg Asn Phe Ser Ile Gln
225 230 235 240

Asp Ser Ser Arg Phe Val Lys Lys Gly Asp Lys Gly Val Asp Leu Val
245 250 255

Ala Ser Leu Cys Lys Ile Tyr Asp Ala Ser Glu Asp Glu Leu Arg Ile
260 265 270

Val Ile Asp Lys Ala Asn Asn Leu Val Glu Thr Ile Leu Lys Lys Lys
275 280 285

Pro Ser Pro Ala Ser Glu Cys Gln Thr Asp Lys Leu Asp Asn Ile Asp
290 295 300

Pro Asp Gly Leu Thr Tyr Phe Glu Asp Leu Leu Glu Glu Thr Ser Ile
305 310 315 320

Ser Thr Ser Leu Ile Thr Leu Glu Lys Asp Tyr Tyr Asp Gly Lys Gly
325 330 335

sequence listing S-92981.ST25

Glu Leu Asp Glu Arg Val Phe Ile Asn Glu Glu Asp Ser Leu Leu Gly
340 345 350

Ser Gly Ser Leu Ser Ala Gly Ala Val Asn Ile Thr Gly Val Lys Arg
355 360 365

Lys Ile Asp Ala Leu Ser Ser Pro Ala Arg Thr Phe Ile Ser Pro Leu
370 375 380

Ser Pro His Lys Ser Pro Ala Ala Lys Thr Asn Gly Ile Ser Gly Ala
385 390 395 400

Thr Lys Leu Ala Ala Thr Pro Val Ser Thr Ala Met Thr Thr Ala Lys
405 410 415

Trp Leu Arg Thr Val Ile Ser Pro Leu Leu Pro Lys Pro Ser Pro Gly
420 425 430

Leu Glu His Phe Leu Lys Ser Cys Asp Arg Asp Ile Thr Asn Asp Val
435 440 445

Thr Arg Arg Ala His Ile Ile Leu Glu Ala Ile Phe Pro Asn Ser Ser
450 455 460

Leu Gly Ala Gln Cys Gly Gly Gly Ser Leu Gln Ala Val Asp Leu Met
465 470 475 480

Asp Asp Ile Trp Ala Glu Gln Arg Arg Leu Glu Ala Cys Lys Leu Tyr
485 490 495

Tyr Arg Val Leu Glu Ala Met Cys Lys Ala Glu Ala Gln Ile Leu His
500 505 510

Ala Asn Asn Leu Asn Ser Leu Leu Thr Asn Glu Arg Phe His Arg Cys
515 520 525

Met Leu Ala Cys Ser Ala Glu Leu Val Leu Ala Thr His Lys Thr Ile
530 535 540

Thr Met Leu Phe Pro Ala Val Leu Glu Arg Thr Gly Ile Thr Ala Phe
545 550 555 560

Asp Leu Ser Lys Val Ile Glu Ser Phe Ile Arg His Glu Asp Ser Leu

sequence listing S-92981.ST25

565

570

575

Pro Arg Glu Leu Arg Arg His Leu Asn Ser Leu Glu Glu Arg Leu Leu
580 585 590

Glu Ser Met Val Trp Glu Lys Gly Ser Ser Met Tyr Asn Ser Leu Ile
595 600 605

Val Ala Arg Pro Ser Leu Ala Leu Glu Ile Asn Gln Leu Gly Leu Leu
610 615 620

Ala Glu Pro Met Pro Ser Leu Asp Ala Ile Ala Ala Leu Ile Asn Phe
625 630 635 640

Ser Asp Gly Ala Asn His Ala Ser Ser Val Gln Lys His Glu Thr Cys
645 650 655

Pro Gly Gln Asn Gly Gly Ile Arg Ser Pro Lys Arg Leu Cys Thr Asp
660 665 670

Tyr Arg Ser Ile Leu Val Glu Arg Asn Ser Phe Thr Ser Pro Val Lys
675 680 685

Asp Arg Leu Leu Ala Leu Gly Asn Val Lys Ser Lys Met Leu Pro Pro
690 695 700

Pro Leu Gln Ser Ala Phe Ala Ser Pro Thr Arg Pro Asn Pro Gly Gly
705 710 715 720

Gly Gly Glu Thr Cys Ala Glu Thr Gly Ile Asn Ile Phe Phe Thr Lys
725 730 735

Ile Asn Lys Leu Ala Ala Val Arg Ile Asn Gly Met Val Glu Arg Leu
740 745 750

Gln Leu Ser Gln Gln Ile Arg Glu Ser Val Tyr Cys Phe Phe Gln His
755 760 765

Val Leu Ala Gln Arg Thr Ser Leu Leu Phe Ser Arg His Ile Asp Gln
770 775 780

Ile Ile Leu Cys Cys Phe Tyr Gly Val Ala Lys Ile Ser Gln Met Ser
785 790 795 800

sequence listing S-92981.ST25

Leu Thr Phe Arg Glu Ile Ile Tyr Asn Tyr Arg Lys Gln Pro Gln Cys
805 810 815

Lys Pro Leu Val Phe Arg Ser Val Tyr Val Asp Ala Leu Gln Cys Arg
820 825 830

Arg Gln Gly Arg Ile Gly Pro Asp His Val Asp Ile Ile Thr Phe Tyr
835 840 845

Asn Glu Ile Phe Ile Pro Ala Val Lys Pro Leu Leu Val Glu Leu Gly
850 855 860

Pro Val Arg Asn Asp Arg Ala Val Glu Ala Asn Asn Lys Pro Glu Gly
865 870 875 880

Gln Cys Pro Gly Ser Pro Lys Val Ser Val Phe Pro Ser Val Pro Asp
885 890 895

Met Ser Pro Lys Lys Val Ser Ala Val His Asn Val Tyr Val Ser Pro
900 905 910

Leu Arg Gly Ser Lys Met Asp Ala Leu Ile Ser His Ser Thr Lys Ser
915 920 925

Tyr Tyr Ala Cys Val Gly Glu Ser Thr His Ala Tyr Gln Ser Pro Ser
930 935 940

Lys Asp Leu Ser Ala Ile Asn Asn Arg Leu Asn Asn Ser Ser Ser Asn
945 950 955 960

Arg Lys Arg Thr Leu Asn Phe Asp Ala Glu Ala Gly Met Val Ser Asp
965 970 975

Ser Met Val Ala Asn Ser Leu Asn Leu Gln Asn Gln Asn Gln Asn Gln
980 985 990

Asn Gly Ser Asp Ala Ser Ser Ser Gly Gly Ala Ala Pro Leu Lys Thr
995 1000 1005

Glu Pro Thr Asp Ser
1010

<210> 3
<211> 4367
<212> DNA

sequence listing S-92981.ST25

<213> Zea mays

<400> 3

tcattctccc	ttcaccccg	gggcgcagg	cgcgctctct	cctcgtggcg	atcgccgacc	60
gtagcggccg	ctgcccgggt	tttcgtcggc	cgcttcgcc	tgtcttcgct	ggacccttcg	120
ccagcgacga	gcacccaaca	gaagcaattg	gagagtttgg	taaatctact	gacgcaggga	180
agcaggttct	accgcaaagc	atataatgaa	ctgttctcag	gtgtaactac	tgagcaggat	240
ccggattcat	cgactaatat	tcctgagtat	atgctttttg	ggtggcatct	cttcttaatg	300
ctccatttga	gacaccaga	attgttcaag	gacctggtgt	cctgcatcca	tggattagtt	360
gctgtgttgg	ccatactttt	gattcacgtg	ccagctaaat	ttaggagctt	cacgattgaa	420
ggctcttctc	acttaatcaa	acaaactgag	aaaggcgtgg	atcttattgc	ttcattatgt	480
cataactatc	atacctctga	agaacgtttg	aaagaaatgt	tgacaagtc	tcacaatgca	540
atagaagaca	ttttccatat	gaaagcacta	agtgttcag	agtgcaaacc	agaaaatttg	600
gataagatag	acacagatga	cctgatgtat	ttcaaaggtc	tgattgatat	ggaatgtttc	660
cagtcaaatt	tggaaaaaat	ggagaaacta	tgtaattcta	atagctgtaa	aggggagctt	720
gattttaaat	caattttgat	caataatgat	tatattccct	atgatgagaa	ctcgacgggg	780
gattccacca	atttaggaca	ttcaaagtgt	gcctttgaaa	cattggcatc	tcccacaaag	840
acaataaaga	acatgctgac	tgttcctagt	tctcctttgt	caccagccac	cggtggttca	900
gtcaagattg	tgcaaatgac	accagtaact	tctgccatga	cgacagctaa	gtggcttcgt	960
gaggtgatat	cttcattgcc	agataagcct	tcattctaagc	ttcagcagtt	tctgtcatca	1020
tgcgataggg	atttgacaaa	tgctgtcaca	gaaaggggtc	gcatagtttt	ggaagcaatt	1080
tttccaacca	aattcttctgc	caatcggggg	gtatcgttag	gtctcaattg	tgcaaatgcc	1140
tttgacattc	cgtgggcaga	agccagaaaa	gtggaggctt	ccaagttgta	ctatagggtg	1200
ttagaggcaa	tctgcagagc	ggagttacaa	aacagcaatg	taaataatct	aactccattg	1260
ctgtcaaatg	agcgtttcca	ccgatgtttg	attgcatgtt	cagcggactt	agtattggcg	1320
acacataaga	cagtcattcat	gatgtttcct	gctgttcttg	agagtaccgg	tctaactgca	1380
tttgatttga	gcaaaataat	tgagaacttt	gtgagacatg	aagagaccct	ccaagagaa	1440
ttgaaaaggc	acctaaattc	cttagaagaa	cagcttttgg	aaagcatggc	atgggagaaa	1500
ggttcatcat	tgtataactc	actgattgtt	gccaggccat	ctgttgcttc	agaaataaac	1560
cgccttggtc	ttttggctga	accaatgcc	tctcttgatg	acttagtgtc	aaggcagaat	1620
gttcgtatcg	agggcttgcc	tgctacacca	tctaaaaaac	gtgctgctgg	tccagatgac	1680

sequence listing S-92981.ST25

aacgctgata ctcgatacacc aaagagatcg tgcaatgaat ctaggaacac agtagtagag	1740
cgcaatttgc agacacctcc acccaagcaa agccacatgg tgtcaactag tttgaaagca	1800
aaatgccatc cactccagtc cacatttgca agtccaactg tctgtaatcc tgttggtggg	1860
aatgaaaaat gtgctgacgt gacaattcat atattctttt ccaagattct gaagttggct	1920
gctattagaa taagaaactt gtgcgaaagg gttcaatgtg tggaacagac agagcgtgac	1980
tataatgtct tcaagcagat tcttgagcaa cagacaacat tattttttta tagacacatc	2040
gatcaactta tcctttgctg tctttatggg gttgcaaagg tttgtcaatt agaactcaca	2100
ttcagggaga tactcaacaa ttacaaaaga gaagcacaat gcaagccaga agttttttca	2160
agtatctata ttgggagtag gaaccgtaat ggggtattag tatcgcgcca tgttggtatc	2220
attacttttt acaatgaggt atttggtcca gcagcgaagc ctttcctggg gtcactaata	2280
tcactctgga ctcatccaga agacaagaag aatgctagtg gccaaattcc tggatcacc	2340
aagccatctc ctttcccaaa ttaccagat atgtcccca agaaagtttc agcatctcat	2400
aatgtatatg tgtctccttt gcggcaaacc aagttggatc tactgctgac accaagttcc	2460
aggagttttt atgcatgcat tgggtgaagg acccatgctt atcagagccc atctaaggat	2520
ttggctgcta taaatagccg cctaaattat aatggcagga aagtaaacag tcgattaaat	2580
ttcgacatgg tgagtgactc agtggttagc ggcagtctgg gccagataaa tgggtggttct	2640
acctcggatc ctgcagctgc atttagcccc ctttcaaaga agagagagac agatacttga	2700
tcaattataa atggtggcct ctctcgtata tagctcacag atccgtgctc cgtagcagtc	2760
tattcttctg aataagtga ttaactggag cgatttaact gtacatgtat gtgttagtga	2820
gaagcagcag tttttaggca gcaaactgtt tcaagttagc ttttgagcta tcaccatttc	2880
tctgctgatt gaacatatcc gctgtgtaga gtgctaata atctttagtt ttcattgggc	2940
tgacataaca aatctttatc ctagtggct ggttggtggg aggcattcat cagggttata	3000
tttggttgtc aaaaagtact gtacttaatt cacatctttc acatttttca ctagcaatag	3060
cagccccaaa ttgctttcct gactaggaac atattcttta cagggtataag catgccaaact	3120
ctaaactata tgaatccttt ttatattctc atttttaagt acttctctgt ttctgctact	3180
tttgtagtgt atatttccag cttctccatc agactgatga tcccatattc agtgtgctgc	3240
aagtgatttg acatatgtgg cttatccttc aggtatgtct catgttggtga cttcattgct	3300
gattgctttt gtaatggtag tgttgagttc atttctgggt acaatcagcc tttactgctt	3360
tatattgttc tactaatttt ggcttgca ggcaggacga ttgggtttct gcatcaatca	3420
atctttttta ggacaagata tttttgtatg ctacacttcc caaattgcaa ttaatccaga	3480

sequence listing S-92981.ST25

```

agtctacctt gttttattct attagttctc agcaacagtg aatgaatatg aatcagtcac 3540
gctgatagat gttcatctgg ttattccaaa caatctgaca tcgcatctct ttctgcaagt 3600
gagatgaaga aaacctgaaa tgctatcacc atttaaaaca ttggcttctg aagttcaggt 3660
gattagcagg agacgttctg acattgccat tgacatgtac ggtagtgatg gcaggagacg 3720
ttcttaaaca gcagctgctc cttcagcttg taatgtctga ttgtattgac caagagcatc 3780
caccttgccct tatggtacta actgaatgag ctggtgacgc tgactcatct gcataatggc 3840
agatgcttaa ccatctttag gagctcatgt catgattcca gctgcaccgt gtgcaaagt 3900
gaaggccctg caagggcttt ccaggccgca ccaatcctgc ttgcttcttg aagatacata 3960
tggtgccacc taaataaaaag ctgtttctgg ttatgtctgt ccttgacatg tcaacagatt 4020
agtgttgggt tgcagtcgtg tgggtgttaa gtcttgaga aggcgagaag tcattgctgc 4080
cagcattgtg tcgtcaggca cagaagtact caaaagtgag agctactttg ttgcgagcaa 4140
acggagggcg atataggttg atagccaatt tcagttctct atatacaagc agcggatttt 4200
gttttagagtt agcttttgag atgcatcatt tctttcacat ctgattctgt gtgttgtaac 4260
tcggagtcgc gtagaagtta gaatgctaac tgacccttaa ttttcaccga ataatttgct 4320
agcgtttttc agtatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 4367

```

<210> 4
 <211> 866
 <212> PRT
 <213> Zea Mays

<400> 4

Met Ser Ser Leu Asp Pro Ser Pro Ala Thr Ser Thr Gln Gln Lys Gln
 1 5 10 15

Leu Glu Ser Leu Val Asn Leu Leu Thr Gln Gly Ser Arg Phe Tyr Arg
 20 25 30

Lys Ala Tyr Asn Glu Leu Phe Ser Gly Val Thr Thr Glu Gln Asp Pro
 35 40 45

Asp Ser Ser Thr Asn Ile Pro Glu Tyr Met Leu Phe Gly Trp His Leu
 50 55 60

Phe Leu Met Leu His Leu Arg Ser Pro Glu Leu Phe Lys Asp Leu Val
 65 70 75 80

sequence listing S-92981.ST25

Ser Cys Ile His Gly Leu Val Ala Val Leu Ala Ile Leu Leu Ile His
85 90 95

Val Pro Ala Lys Phe Arg Ser Phe Thr Ile Glu Gly Ser Ser His Leu
100 105 110

Ile Lys Gln Thr Glu Lys Gly Val Asp Leu Ile Ala Ser Leu Cys His
115 120 125

Asn Tyr His Thr Ser Glu Glu Arg Leu Lys Glu Met Leu His Lys Ser
130 135 140

His Asn Ala Ile Glu Asp Ile Phe His Met Lys Ala Leu Ser Ala Ser
145 150 155 160

Glu Cys Lys Pro Glu Asn Leu Asp Lys Ile Asp Thr Asp Asp Leu Met
165 170 175

Tyr Phe Lys Gly Leu Ile Asp Met Glu Cys Phe Gln Ser Asn Leu Glu
180 185 190

Lys Met Glu Lys Leu Cys Asn Ser Asn Ser Cys Lys Gly Glu Leu Asp
195 200 205

Phe Lys Ser Ile Leu Ile Asn Asn Asp Tyr Ile Pro Tyr Asp Glu Asn
210 215 220

Ser Thr Gly Asp Ser Thr Asn Leu Gly His Ser Lys Cys Ala Phe Glu
225 230 235 240

Thr Leu Ala Ser Pro Thr Lys Thr Ile Lys Asn Met Leu Thr Val Pro
245 250 255

Ser Ser Pro Leu Ser Pro Ala Thr Gly Gly Ser Val Lys Ile Val Gln
260 265 270

Met Thr Pro Val Thr Ser Ala Met Thr Thr Ala Lys Trp Leu Arg Glu
275 280 285

Val Ile Ser Ser Leu Pro Asp Lys Pro Ser Ser Lys Leu Gln Gln Phe
290 295 300

Leu Ser Ser Cys Asp Arg Asp Leu Thr Asn Ala Val Thr Glu Arg Val
305 310 315 320

sequence listing S-92981.ST25

Ser Ile Val Leu Glu Ala Ile Phe Pro Thr Lys Ser Ser Ala Asn Arg
325 330 335

Gly Val Ser Leu Gly Leu Asn Cys Ala Asn Ala Phe Asp Ile Pro Trp
340 345 350

Ala Glu Ala Arg Lys Val Glu Ala Ser Lys Leu Tyr Tyr Arg Val Leu
355 360 365

Glu Ala Ile Cys Arg Ala Glu Leu Gln Asn Ser Asn Val Asn Asn Leu
370 375 380

Thr Pro Leu Leu Ser Asn Glu Arg Phe His Arg Cys Leu Ile Ala Cys
385 390 395 400

Ser Ala Asp Leu Val Leu Ala Thr His Lys Thr Val Ile Met Met Phe
405 410 415

Pro Ala Val Leu Glu Ser Thr Gly Leu Thr Ala Phe Asp Leu Ser Lys
420 425 430

Ile Ile Glu Asn Phe Val Arg His Glu Glu Thr Leu Pro Arg Glu Leu
435 440 445

Lys Arg His Leu Asn Ser Leu Glu Glu Gln Leu Leu Glu Ser Met Ala
450 455 460

Trp Glu Lys Gly Ser Ser Leu Tyr Asn Ser Leu Ile Val Ala Arg Pro
465 470 475 480

Ser Val Ala Ser Glu Ile Asn Arg Leu Gly Leu Leu Ala Glu Pro Met
485 490 495

Pro Ser Leu Asp Asp Leu Val Ser Arg Gln Asn Val Arg Ile Glu Gly
500 505 510

Leu Pro Ala Thr Pro Ser Lys Lys Arg Ala Ala Gly Pro Asp Asp Asn
515 520 525

Ala Asp Pro Arg Ser Pro Lys Arg Ser Cys Asn Glu Ser Arg Asn Thr
530 535 540

Val Val Glu Arg Asn Leu Gln Thr Pro Pro Pro Lys Gln Ser His Met
545 550 555 560

sequence listing S-92981.ST25

Val Ser Thr Ser Leu Lys Ala Lys Cys His Pro Leu Gln Ser Thr Phe
565 570 575

Ala Ser Pro Thr Val Cys Asn Pro Val Gly Gly Asn Glu Lys Cys Ala
580 585 590

Asp Val Thr Ile His Ile Phe Phe Ser Lys Ile Leu Lys Leu Ala Ala
595 600 605

Ile Arg Ile Arg Asn Leu Cys Glu Arg Val Gln Cys Val Glu Gln Thr
610 615 620

Glu Arg Val Tyr Asn Val Phe Lys Gln Ile Leu Glu Gln Gln Thr Thr
625 630 635 640

Leu Phe Phe Asn Arg His Ile Asp Gln Leu Ile Leu Cys Cys Leu Tyr
645 650 655

Gly Val Ala Lys Val Cys Gln Leu Glu Leu Thr Phe Arg Glu Ile Leu
660 665 670

Asn Asn Tyr Lys Arg Glu Ala Gln Cys Lys Pro Glu Val Phe Ser Ser
675 680 685

Ile Tyr Ile Gly Ser Thr Asn Arg Asn Gly Val Leu Val Ser Arg His
690 695 700

Val Gly Ile Ile Thr Phe Tyr Asn Glu Val Phe Val Pro Ala Ala Lys
705 710 715 720

Pro Phe Leu Val Ser Leu Ile Ser Ser Gly Thr His Pro Glu Asp Lys
725 730 735

Lys Asn Ala Ser Gly Gln Ile Pro Gly Ser Pro Lys Pro Ser Pro Phe
740 745 750

Pro Asn Leu Pro Asp Met Ser Pro Lys Lys Val Ser Ala Ser His Asn
755 760 765

Val Tyr Val Ser Pro Leu Arg Gln Thr Lys Leu Asp Leu Leu Leu Ser
770 775 780

Pro Ser Ser Arg Ser Phe Tyr Ala Cys Ile Gly Glu Gly Thr His Ala

sequence listing S-92981.ST25

785 790 795 800

Tyr Gln Ser Pro Ser Lys Asp Leu Ala Ala Ile Asn Ser Arg Leu Asn
805 810 815

Tyr Asn Gly Arg Lys Val Asn Ser Arg Leu Asn Phe Asp Met Val Ser
820 825 830

Asp Ser Val Val Ala Gly Ser Leu Gly Gln Ile Asn Gly Gly Ser Thr
835 840 845

Ser Asp Pro Ala Ala Ala Phe Ser Pro Leu Ser Lys Lys Arg Glu Thr
850 855 860

Asp Thr
865

<210> 5
<211> 2945
<212> DNA
<213> Zea mays

<400> 5
gagaattgaa aagacaccta aattccttag aagaacaaat ttgggaaagc atggcatggg 60
agaaagggttc atcattgtat aactcactga ttgttgccag gccatctgtt gcttcagaaa 120
ttaatcgctt tggctctctg gctgaatcaa tgccatctct tgatgactta gtggcaaggc 180
agaatattca tattgagggc ttgcttgcta caccatctaa aaaacgtgct gctggtcgag 240
acgacaatgc tgatcctcga tcaccaaaga gaccatgcaa tgaatctagg agcacagtag 300
tagaacacaa ttgagcagaca cctccacca agcaatgcca catggtgttg actagtttga 360
aagcaaaatg ccatccactc cagtccacat ttgcaagtcc aactgtcagt aatcctgttg 420
gtgggaacga aaaatgtgct gacgtgacaa ttcagatatt cttttccaaa attctgaagt 480
tagctgctat tagaataaga aacttgtgtg aaaggattca atatatggaa cagacagagc 540
gtgtctataa tgtcttcaag cagattcttg atcaacagac aacattatct tttaatagac 600
acatgcatca acttattctt tgctgtcttt atggtgttgc aaaggtttgc caattagaac 660
tctcattcag ggagatactc aacaattaca aaaaagaagc acaatgcaaa ccagaagttt 720
ttttaagcat ctatattgga agtaggaatc ataatggggt attaatatca cgccatgttg 780
atatcattac tttttacaat gaggtctttg ttccagcagc caagcctttc ctggtgtcat 840
taatatcatc tgggtactcg ccagaagaca agaagaatgc tagtggccaa gttcctggat 900

sequence listing S-92981.ST25

caccgaagct atctcctttc ccaaatttac cagatatgtc ccaaagaaa gtttcagctt	960
ctcataatgt atatgtgtct cctttgcggc aaaccaagat ggatttactg ctgtcaccaa	1020
gttcaggag tttttatgca tgcattggtg aaggcaccca tgcttatcag agcccatcta	1080
aagatttggc tgctataaat agccgcctaa attataatgg tcggagagta aacagtcgat	1140
taaactttga catggtgagc gactcagtg tagctggtag tctaggccag ccaaattggtg	1200
gttctacttc cttggatcct gcagctgcat ttagccccct ttcaaagaga aagccagata	1260
cttgatcaaa tataaatggc gatctctctc gtatatagct cacagctcca tagcagtcta	1320
ttcttctgaa taagtgggtt gactggagtg atttaactgt acatgtatgt gttagtgaga	1380
accagcagtt tataggcagc aaactgtttt aaattagctt tgaggtttta tcaccatttc	1440
cctgctgatt gaacatatat tagattgtaa catctgcttt gtagaatgct aatgaatctt	1500
tagttttcag tgggttgaca ttaaaaatcc ttatcctagt tggctggttg ttgggagaca	1560
ttcatcaagg ttatatattg tcgtcaaata gtactgtact tgattcatat ctttcatatt	1620
tttactagc gttggcaacc gtaaattgct ttcttgacta ggaacatatt cttcacaagt	1680
atggcaactc taaactatit gaccttttat attctcattt ttaagtactt tctctatttc	1740
tgctactttt gtactgtgta tttccagctt ctccaccaga ctgattgtta gagtgtatgc	1800
tcctatatta tccatgtatg tgtaaatggg ctgctagccc attagggtta ggttcccctg	1860
ggcttatata tgtaaccacc ctctatgcaa tagaagttga atatcagttt ctatcactaa	1920
tgattccata ttcagtgggc tgcaagtgat ttgacatacg tgccttatcc ttcaggtatg	1980
tctcatgttg actttgcttt tgtaattgga ctgttggtt cattgctgga atgctgggta	2040
taatcaacct ttactgtct atattgttct ttttttggtt tgcacaacca ggggtggttg	2100
ttttctgaat caatcaatcc atttcctcgg acgacaagat aatttttgta tgttacctt	2160
ccaaaattg caattaattc agaagtctgc ctactttcat tcagttagtt ctcagcaaca	2220
ctgaaaggat atgaatcagt caaccgata gatgtttatc tggttattcc aaacaatctg	2280
acatcacatc tgtttctgca ggcgagataa ggaaaatctg aaatgctatc accatttaaa	2340
acattggctc ctggaagttc aggtaggtgt tgctgtagaa tgagatggtt aggaatcttt	2400
acaagctcag gctatatgat ttcagcagca ctgtaacctg gggtgcaa atgttaaggccc	2460
tgcaagcact ttccaggcca caccaattct gcttggttct tgaagatata ttcttcctat	2520
gtgcccccta tataaaagcc atttctggtt gttatgttta tccttgacat gtcaacagat	2580
tagtggtggg ttgcagtcac gcggtcctta agtctcggag aaggcgagaa gtcattgctg	2640
ctagcattgt gatcgtcggc cagcaaagta atcaaaaagt gagagctact tgttcctagc	2700

sequence listing S-92981.ST25

aaatggagaa gggcgatata taggtttatg atcaaattca gtgtatgcaa gcagcatatt 2760
 ttgttttagag ttagcttttg aggttcatca tttcatttca cagctgattc tctatgttgt 2820
 aactccttag tcgtgtagaa attagaatgc tatctgctta attttttagtg aataatttgc 2880
 tagtatattt ttgaatgtaa ttgcagtagc tctgcctctt cattaaggaa aaaaaaaaaa 2940
 aaaaaa 2945

<210> 6
 <211> 420
 <212> PRT
 <213> Zea mays
 <400> 6

Glu Leu Lys Arg His Leu Asn Ser Leu Glu Glu Gln Ile Leu Glu Ser
 1 5 10 15
 Met Ala Trp Glu Lys Gly Ser Ser Leu Tyr Asn Ser Leu Ile Val Ala
 20 25 30
 Arg Pro Ser Val Ala Ser Glu Ile Asn Arg Phe Gly Leu Leu Ala Glu
 35 40 45
 Ser Met Pro Ser Leu Asp Asp Leu Val Ala Arg Gln Asn Ile His Ile
 50 55 60
 Glu Gly Leu Pro Ala Thr Pro Ser Lys Lys Arg Ala Ala Gly Arg Asp
 65 70 75 80
 Asp Asn Ala Asp Pro Arg Ser Pro Lys Arg Pro Cys Asn Glu Ser Arg
 85 90 95
 Ser Thr Val Val Glu His Asn Leu Gln Thr Pro Pro Pro Lys Gln Cys
 100 105 110
 His Met Val Leu Thr Ser Leu Lys Ala Lys Cys His Pro Leu Gln Ser
 115 120 125
 Thr Phe Ala Ser Pro Thr Val Ser Asn Pro Val Gly Gly Asn Glu Lys
 130 135 140
 Cys Ala Asp Val Thr Ile Gln Ile Phe Phe Ser Lys Ile Leu Lys Leu
 145 150 155 160

sequence listing S-92981.ST25

Ala Ala Ile Arg Ile Arg Asn Leu Cys Glu Arg Ile Gln Tyr Met Glu
165 170 175

Gln Thr Glu Arg Val Tyr Asn Val Phe Lys Gln Ile Leu Asp Gln Gln
180 185 190

Thr Thr Leu Phe Phe Asn Arg His Met His Gln Leu Ile Leu Cys Cys
195 200 205

Leu Tyr Gly Val Ala Lys Val Cys Gln Leu Glu Leu Ser Phe Arg Glu
210 215 220

Ile Leu Asn Asn Tyr Lys Lys Glu Ala Gln Cys Lys Pro Glu Val Phe
225 230 235 240

Leu Ser Ile Tyr Ile Gly Ser Arg Asn His Asn Gly Val Leu Ile Ser
245 250 255

Arg His Val Asp Ile Ile Thr Phe Tyr Asn Glu Val Phe Val Pro Ala
260 265 270

Ala Lys Pro Phe Leu Val Ser Leu Ile Ser Ser Gly Thr Arg Pro Glu
275 280 285

Asp Lys Lys Asn Ala Ser Gly Gln Val Pro Gly Ser Pro Lys Leu Ser
290 295 300

Pro Phe Pro Asn Leu Pro Asp Met Ser Pro Lys Lys Val Ser Ala Ser
305 310 315 320

His Asn Val Tyr Val Ser Pro Leu Arg Gln Thr Lys Met Asp Leu Leu
325 330 335

Leu Ser Pro Ser Ser Arg Ser Phe Tyr Ala Cys Ile Gly Glu Gly Thr
340 345 350

His Ala Tyr Gln Ser Pro Ser Lys Asp Leu Ala Ala Ile Asn Ser Arg
355 360 365

Leu Asn Tyr Asn Gly Arg Arg Val Asn Ser Arg Leu Asn Phe Asp Met
370 375 380

Val Ser Asp Ser Val Val Ala Gly Ser Leu Gly Gln Pro Asn Gly Gly
385 390 395 400

sequence listing S-92981.ST25

Ser Thr Ser Leu Asp Pro Ala Ala Ala Phe Ser Pro Leu Ser Lys Arg
405 410 415

Lys Pro Asp Thr
420

<210> 7
<211> 2538
<212> DNA
<213> Zea mays

<400> 7
cctagtcccc ctttgtcacc caccaacggt ggttcagtca agattgtgca aatgacacca 60
ataaacttctg ccatgacgac agctaagtgg cttcgtgagg tgatatcttc attgccagag 120
aagccttcat ctaagcttca gcagttgatg tcatcatgcg atagagattt gacaaatgcc 180
gtcacagaaa gggtcagcat agttctggaa gcaatttttc caaccaagtc ttctgctgat 240
cggggtggct cattaggcct caattgtgca aatgcctttg atactctatg ggcagatgcc 300
agaaaaatgg aggccttccaa gttgtactat aggggtattag aggcaatctg cagagctgag 360
ttacaaaaca gcaatgtaaa caatctaact ccattgctgt caaatgagcg ttttcaccga 420
tgtttgattg catgttcagc ggagctagta ttggcgacac ataagacggt catcatgatg 480
tttctgctg ttcttgagag tactggtcta acctcatttg atttgagcaa aataattgag 540
aactttgtga gacatgaaga gaccctccca agagaattga aaagacacct aaattcctta 600
gaagaacaaa ttttggaag catggcatgg gagaaagggt catcattgta taactcactg 660
attgttgcca ggccatctgt tgcttcagaa attaatcgct ttggtcttct ggctgaatca 720
atgccatctc ttgatgactt agtggcaagg cagaatattc atattgaggg cttgcctgct 780
acaccatcta aaaaacgtgc tgctggtcga gacgacaatg ctgatcctcg atcaccaaag 840
agaccatgca atgaatctag gagcacagta gtagaacaca atttgcagac acctccaccc 900
aagcaatgcc acatgggtgtt gactagtttg aaagcaaaat gccatccact ccagtccaca 960
tttgcaagtc caactgtcag taatcctggt ggtgggaacg aaaaatgtgc tgacgtgaca 1020
attcagatat tcttttccaa aattctgaag ttagctgcta ttagaataag aaacttgtgt 1080
gaaaggattc aatatatgga acagacagag cgtgtctata atgtcttcaa gcagattctt 1140
gatcaacaga caacattatt ttttaataga cacatgcadc aacttattct ttgctgtctt 1200
tatggtgttg caaagggttg ccaattagaa ctctcattca gggagatact caacaattac 1260
aaaaaagaag cacaatgcaa accagaagtt tttttaagca tctatattgg aagtaggaat 1320

sequence listing S-92981.ST25

cataatgggg tattaatatc acgccatggt gatatacatta ctttttacaa tgaggtcttt 1380
gttccagcag ccaagccttt cctggtgtca ttaatatcat ctggtactcg tccagaagac 1440
aagaagaatg ctagtggcca agttcctgga tcaccgaagc tatctccttt cccaaattta 1500
ccagatatgt ccccaaagaa agtttcagct tctcataatg tataatgtgtc tcctttgcgg 1560
caaaccaaga tggatttact gctgtcacca agttccagga gtttttatgc atgcattggt 1620
gaaggcacc atgcttatca gagcccatct aaagatttgg ctgctataaa tagccgccta 1680
aattataatg gtcggagagt aaacagtcga ttaaactttg acatgggatg tctcatgttg 1740
actttgcttt tgtaatggta ctggttgctt cattgctgga atgctggta taatcaacct 1800
ttactgctct atattgttct ttttttggtt tgcacaacca ggggtggttg ttttctgaat 1860
caatcaatcc atttcctcgg acacaagata atttttgcga gataaggaaa atctgaaatg 1920
ctatcaccat ttaaaacatt ggctcctgga agttcaggtt aggtgttgct gtagaatgag 1980
atggttacca tctttacaag ctgaggctat atgatttcag cagcactgta acctgggggtg 2040
caaatgttaa ggccctgcaa gcactttcca ggccacacca attctgcttg gttcttgaag 2100
atacattctt cctatgtgcc ccctatataa aagccatttc tggttgttat gtttatcctt 2160
gacatgtcaa cagattagtg ttgggttgca gtcatgcggt ccttaagtct cggagaaggc 2220
gagaagtcac tgctgctagc attgtgatcg tcggccacga aagtaatcaa aaagtgaag 2280
ctacttgctc ctgacaaatg gagaagggcg atatataggt ttatgatcaa attcagtgt 2340
tgcaagcagc atattttgtt tagagttagc ttttgaggtt catcatttca tttcacagct 2400
gattctctat gttgtaactc cttagtcgtg tagaaattag aatgctatct gcttaatttt 2460
tagtgaataa tttgctagta ttttttgaa tgtaattgca gtagctctgc ctcttcatta 2520
aaaaaaaaa aaaaaaaaaa 2536

<210> 8
<211> 584
<212> PRT
<213> Zea mays

<400> 8

Pro Ser Ser Pro Leu Ser Pro Thr Asn Gly Gly Ser Val Lys Ile Val
1 5 10 15

Gln Met Thr Pro Ile Thr Ser Ala Met Thr Thr Ala Lys Trp Leu Arg
20 25 30

Glu Val Ile Ser Ser Leu Pro Glu Lys Pro Ser Ser Lys Leu Gln Gln

sequence listing S-92981.ST25

35

40

45

Leu Met Ser Ser Cys Asp Arg Asp Leu Thr Asn Ala Val Thr Glu Arg
50 55 60

Val Ser Ile Val Leu Glu Ala Ile Phe Pro Thr Lys Ser Ser Ala Asp
65 70 75 80

Arg Gly Gly Ser Leu Gly Leu Asn Cys Ala Asn Ala Phe Asp Thr Leu
85 90 95

Trp Ala Asp Ala Arg Lys Met Glu Ala Ser Lys Leu Tyr Tyr Arg Val
100 105 110

Leu Glu Ala Ile Cys Arg Ala Glu Leu Gln Asn Ser Asn Val Asn Asn
115 120 125

Leu Thr Pro Leu Leu Ser Asn Glu Arg Phe His Arg Cys Leu Ile Ala
130 135 140

Cys Ser Ala Glu Leu Val Leu Ala Thr His Lys Thr Val Ile Met Met
145 150 155 160

Phe Pro Ala Val Leu Glu Ser Thr Gly Leu Thr Ser Phe Asp Leu Ser
165 170 175

Lys Ile Ile Glu Asn Phe Val Arg His Glu Glu Thr Leu Pro Arg Glu
180 185 190

Leu Lys Arg His Leu Asn Ser Leu Glu Glu Gln Ile Leu Glu Ser Met
195 200 205

Ala Trp Glu Lys Gly Ser Ser Leu Tyr Asn Ser Leu Ile Val Ala Arg
210 215 220

Pro Ser Val Ala Ser Glu Ile Asn Arg Phe Gly Leu Leu Ala Glu Ser
225 230 235 240

Met Pro Ser Leu Asp Asp Leu Val Ala Arg Gln Asn Ile His Ile Glu
245 250 255

Gly Leu Pro Ala Thr Pro Ser Lys Lys Arg Ala Ala Gly Arg Asp Asp
260 265 270

sequence listing S-92981.ST25

Asn Ala Asp Pro Arg Ser Pro Lys Arg Pro Cys Asn Glu Ser Arg Ser
275 280 285

Thr Val Val Glu His Asn Leu Gln Thr Pro Pro Pro Lys Gln Cys His
290 295 300

Met Val Leu Thr Ser Leu Lys Ala Lys Cys His Pro Leu Gln Ser Thr
305 310 315 320

Phe Ala Ser Pro Thr Val Ser Asn Pro Val Gly Gly Asn Glu Lys Cys
325 330 335

Ala Asp Val Thr Ile Gln Ile Phe Phe Ser Lys Ile Leu Lys Leu Ala
340 345 350

Ala Ile Arg Ile Arg Asn Leu Cys Glu Arg Ile Gln Tyr Met Glu Gln
355 360 365

Thr Glu Arg Val Tyr Asn Val Phe Lys Gln Ile Leu Asp Gln Gln Thr
370 375 380

Thr Leu Phe Phe Asn Arg His Met His Gln Leu Ile Leu Cys Cys Leu
385 390 395 400

Tyr Gly Val Ala Lys Val Cys Gln Leu Glu Leu Ser Phe Arg Glu Ile
405 410 415

Leu Asn Asn Tyr Lys Lys Glu Ala Gln Cys Lys Pro Glu Val Phe Leu
420 425 430

Ser Ile Tyr Ile Gly Ser Arg Asn His Asn Gly Val Leu Ile Ser Arg
435 440 445

His Val Asp Ile Ile Thr Phe Tyr Asn Glu Val Phe Val Pro Ala Ala
450 455 460

Lys Pro Phe Leu Val Ser Leu Ile Ser Ser Gly Thr Arg Pro Glu Asp
465 470 475 480

Lys Lys Asn Ala Ser Gly Gln Val Pro Gly Ser Pro Lys Leu Ser Pro
485 490 495

Phe Pro Asn Leu Pro Asp Met Ser Pro Lys Lys Val Ser Ala Ser His
500 505 510

sequence listing S-92981.ST25

Asn Val Tyr Val Ser Pro Leu Arg Gln Thr Lys Met Asp Leu Leu Leu
515 520 525

Ser Pro Ser Ser Arg Ser Phe Tyr Ala Cys Ile Gly Glu Gly Thr His
530 535 540

Ala Tyr Gln Ser Pro Ser Lys Asp Leu Ala Ala Ile Asn Ser Arg Leu
545 550 555 560

Asn Tyr Asn Gly Arg Arg Val Asn Ser Arg Leu Asn Phe Asp Met Val
565 570 575

Cys Leu Met Leu Thr Leu Leu Leu
580

<210> 9
<211> 6422
<212> DNA
<213> Arabidopsis Thaliana

<220>
<221> promoter
<222> (1)..(543)
<223>

<220>
<221> 5'UTR
<222> (544)..(653)
<223>

<220>
<221> Intron
<222> (654)..(1093)
<223>

<220>
<221> 5'UTR
<222> (1094)..(1107)
<223>

<220>
<221> exon
<222> (1108)..(1189)
<223>

<220>
<221> Intron
<222> (1190)..(1307)

sequence listing S-92981.ST25

<223>

<220>

<221> exon

<222> (1308)..(1410)

<223>

<220>

<221> Intron

<222> (1411)..(1497)

<223>

<220>

<221> exon

<222> (1498)..(1641)

<223>

<220>

<221> Intron

<222> (1642)..(1721)

<223>

<220>

<221> exon

<222> (1722)..(1817)

<223>

<220>

<221> Intron

<222> (1818)..(1902)

<223>

<220>

<221> exon

<222> (1903)..(1951)

<223>

<220>

<221> Intron

<222> (1952)..(2216)

<223>

<220>

<221> exon

<222> (2217)..(2409)

<223>

<220>

<221> Intron

sequence listing S-92981.ST25

<222> (2410)..(2540)
<223>

<220>
<221> exon
<222> (2541)..(2606)
<223>

<220>
<221> Intron
<222> (2607)..(2693)
<223>

<220>
<221> exon
<222> (2694)..(2873)
<223>

<220>
<221> Intron
<222> (2874)..(2973)
<223>

<220>
<221> exon
<222> (2974)..(4029)
<223>

<220>
<221> Intron
<222> (4030)..(4124)
<223>

<220>
<221> exon
<222> (4125)..(4287)
<223>

<220>
<221> Intron
<222> (4288)..(4385)
<223>

<220>
<221> exon
<222> (4386)..(4458)
<223>

<220>

sequence listing S-92981.ST25

<221> Intron
<222> (4459)..(4579)
<223>

<220>
<221> exon
<222> (4580)..(4756)
<223>

<220>
<221> Intron
<222> (4757)..(4869)
<223>

<220>
<221> exon
<222> (4870)..(4969)
<223>

<220>
<221> Intron
<222> (4970)..(5051)
<223>

<220>
<221> exon
<222> (5052)..(5184)
<223>

<220>
<221> Intron
<222> (5185)..(5276)
<223>

<220>
<221> exon
<222> (5277)..(5390)
<223>

<220>
<221> Intron
<222> (5391)..(5497)
<223>

<220>
<221> exon
<222> (5498)..(5613)
<223>

sequence listing S-92981.ST25

<220>
 <221> Intron
 <222> (5614)..(5695)
 <223>

<220>
 <221> exon
 <222> (5696)..(5870)
 <223>

<220>
 <221> 3'UTR
 <222> (5871)..(6081)
 <223>

<220>
 <221> misc_feature
 <222> (6082)..(6421)
 <223>

<400> 9
 gatcctactc acactcgaag atgacgaaga agacttaatc tgaatccatc cgcggatagg 60
 acactcatac ttctgcaacc aaacgttcta caatggcaaa tatgtaattt cccgcgtgac 120
 ctaaactaga aacggcatcg tattaagggt gggcccaatc ataactcaca cgaggctttg 180
 tcgcggtcac gaaaaccag acggcgtaa tggccactc cgtttgtttc gaccccgccg 240
 tgacggcgaa tctttccctc tcagcgtttc acgcaacagt aagtaagttt tggcggtaaa 300
 attgggtcac agatgggtac gtgtcgattt aatagtgggt gaaagcgcgc gaatataatt 360
 gtatacgtat gtgtatgtat tctccgtgtt gtttttcccg cgcgagatat atcctttttt 420
 agggtttgcc gcataatcag accccattct agagagagaa gagggaagtc aggtgaagat 480
 agagagagac actgagagga gggaaaattt gtagggtttc cggagatctc tgtgattcct 540
 ctgaatttgt cgaatttttt ggaggaggcg ttagaagtcg ggcttcttaa aaatcagatc 600
 ttctgctcag cttaaatcgg cgacgtctgg tattgggac tgtgacacaa aaaggtaaga 660
 tctttctcta ttgcctatcc ttgatttga aatcttatcc tctaggtggt ttatctgaaa 720
 ttttctattg atatttcgct attcgattgt aagttgggtg gagaattctc caaaaacaaa 780
 aaagagaaaa actttgaatg aatatttaag ataacatctg ggtaaaattt ttccggagtg 840
 gtgggtttta gattatgcc caatttctct tctttttttt ccccaaattt tgtctttctg 900
 ccatgttttg ggaaattggg agtttgtttt ctcagtgtctg ttagtgtgtt cttccgaatg 960
 ggttgggcat ggttcctatt gaatttcagt gtgattaaat taacaaatct ctttgcttga 1020

sequence listing S-92981.ST25

aaagtcctt tttcttcgtc ttcagtttagc agtttaattg gaagtaaaat tagcttgatt	1080
ttgcatgttt tcagctgcgt tggagac tat gga aga agt tca gcc tcc agt gac	1134
Tyr Gly Arg Ser Ser Ala Ser Ser Asp	
1 5	
ccc gcc cat tga acc aaa tgg gaa aag aag cga agc ctc tct ctt gga	1182
Pro Ala His Thr Lys Trp Glu Lys Lys Arg Ser Leu Ser Leu Gly	
10 15 20	
cat atg c gaggtttact cttctctttg ctgatctagt tgcatttggt tagttgaaga	1239
His Met	
25	
taccatttga gttctctcgg aaattttgag gactagctct aatccctgta gttgatttct	1299
tattgcag aa agt tct gtc tct tga tgg gag cac ttg cga tga agc ttt	1348
Gln Ser Ser Val Ser Trp Glu His Leu Arg Ser Phe	
30 35	
gaa gtt gtt tac aga aac caa acg aat ttt gtc agc aag cat gtc taa	1396
Glu Val Val Tyr Arg Asn Gln Thr Asn Phe Val Ser Lys His Val	
40 45 50	
cat tgg aag tgg aa cgggtgaaata catttttctt ctaacttctc ttttatcagt	1450
His Trp Lys Trp Lys	
55	
taactgtggt ttcattatga ctaaatacctt ttttcttctt cttatta g cgg gaa gaa	1507
Arg Glu Glu	
60	
gta gag agg ttc tgg ttt gcg ttt att ctc tat tca gtg aag agg ctt	1555
Val Glu Arg Phe Trp Phe Ala Phe Ile Leu Tyr Ser Val Lys Arg Leu	
65 70 75	
agt gtg aga aaa gaa gcg gat ggt ctg tca gtg tct ggt gat aat gag	1603
Ser Val Arg Lys Glu Ala Asp Gly Leu Ser Val Ser Gly Asp Asn Glu	
80 85 90	
ttt aat cta tgt cag ata ctg agg gct ctg aag cta aa gtaagtagtg	1651
Phe Asn Leu Cys Gln Ile Leu Arg Ala Leu Lys Leu Lys	
95 100 105	
ttcaattctt ccttccttgt cattcttaaa ttcatttgta gtgacgattt tcctcttttc	1711
tgtttatagt a ttg tgg att ttt tta aag agt tac ctc agt ttg tgg tca	1761
Leu Trp Ile Phe Leu Lys Ser Tyr Leu Ser Leu Trp Ser	
110 115	
agg ctg gat ctg tac tgg gtg aac ttt acg gcg cag act ggg aga aca	1809
Arg Leu Asp Leu Tyr Trp Val Asn Phe Thr Ala Gln Thr Gly Arg Thr	
120 125 130 135	
gac ttc ag gttttgacta acatctttta aatatacttc tacttctatt	1857
Asp Phe Arg	
atatcattgt taaatatgct tctattaact aatttttact tacta g gca aag gag	1912

sequence listing S-92981.ST25
Ala Lys Glu
140

gtg cag gct aac ttt gtg cat ctt agc ctt cta agc aag tgagtttagc Val Gln Ala Asn Phe Val His Leu Ser Leu Leu Ser Lys <div style="display: flex; justify-content: space-between; width: 100%;"> 145 150 </div>	1961
tcccttccta ttttacattt atctttgttt tgtgtaagaa tagttattga catagatttc 	2021
atattttgga cctgcaactt agaagcaaat tttcttccta tgcaataatc agaatatggg 	2081
cttgcaatat tccttcatt ttaaattaat taagatttag agttacagat ttctggtttt 	2141
catgtgatta tattctgtga attgttttaa ggacatgtta aagtatgatg ttttgggtac 	2201
ctttccttgg taaca gat act aca aac gtg ggt tcc ggg aat tct ttt tga <div style="display: flex; justify-content: space-between; width: 100%;"> Asp Thr Thr Asn Val Gly Ser Gly Asn Ser Phe </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 155 160 165 </div>	2252
cat atg atg caa acg cag aaa aga act cag caa act ctt cta cct att His Met Met Gln Thr Gln Lys Arg Thr Gln Gln Thr Leu Leu Pro Ile <div style="display: flex; justify-content: space-between; width: 100%;"> 170 175 180 </div>	2300
tgc tgg ata gtt atc gtt ttg gat ggc tac tct ttt tgg cac tcc gaa Cys Trp Ile Val Ile Val Leu Asp Gly Tyr Ser Phe Trp His Ser Glu <div style="display: flex; justify-content: space-between; width: 100%;"> 185 190 195 </div>	2348
acc atg cgt tta gtc gat tta agg acc tcg tga cat gct caa atg gcg Thr Met Arg Leu Val Asp Leu Arg Thr Ser His Ala Gln Met Ala <div style="display: flex; justify-content: space-between; width: 100%;"> 200 205 210 </div>	2396
tag ttt cta tat t ggtagtgac tacctgtgga gctctccta atctttcatt Phe Leu Tyr <div style="display: flex; justify-content: space-between; width: 100%;"> 215 </div>	2449
catttttagtc ttgctgtaca ttattacttg aaagatgctt cgtttaatat aacgcaattg 	2509
aagtatagge taactccttt tcatgttatc a gg cta ttt tga tca tac atg <div style="display: flex; justify-content: space-between; width: 100%;"> Trp Leu Phe Ser Tyr Met </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 220 </div>	2560
ttc ctt gtc ggt tta gaa att tca gca tcc aag att ctt ctc gct t Phe Leu Val Gly Leu Glu Ile Ser Ala Ser Lys Ile Leu Leu Ala <div style="display: flex; justify-content: space-between; width: 100%;"> 225 230 235 </div>	2606
tggtagagtgt ttatcttttc ttctatcccg ataaccatgg caccatagaa tgtttatcat 	2666
ctattttcat ttatgtgatg aatctca gt taa gaa agg tga caa agg tgt aga <div style="display: flex; justify-content: space-between; width: 100%;"> Cys Glu Arg Gln Arg Cys Arg </div> <div style="display: flex; justify-content: space-between; width: 100%;"> 240 </div>	2719
ctt ggt tgc atc act ttg caa gat ata tga cgc ctc aga aga tga gtt Leu Gly Cys Ile Thr Leu Gln Asp Ile Arg Leu Arg Arg Val <div style="display: flex; justify-content: space-between; width: 100%;"> 245 250 255 </div>	2767
gag gat agt aat tga caa ggc aaa taa ttt ggt aga aac cat act gaa Glu Asp Ser Asn Gln Gly Lys Phe Gly Arg Asn His Thr Glu <div style="display: flex; justify-content: space-between; width: 100%;"> 260 265 270 </div>	2815

sequence listing S-92981.ST25

gaa aaa gcc atc tcc agc atc tga gtg cca aac tga caa gct aga taa	2863
Glu Lys Ala Ile Ser Ser Ile Val Pro Asn Gln Ala Arg	
275 280	
tat tga ccc a gggttggtcta aaatcatttt ccttcttcaa ttaaagaatc	2913
Tyr Pro	
285	
atgtgagttc attgaacagt tgcctgattg ttcttcgaat ctatatgggtg ttttactgca	2973
ga tgg ctt gac cta ctt tga gga ttt act gga aga gac gtc cat ctc	3020
Arg Trp Leu Asp Leu Leu Gly Phe Thr Gly Arg Asp Val His Leu	
290 295 300	
aac tag ctt aat tac act tga aaa gga tta cta tga tgg taa agg cga	3068
Asn Leu Asn Tyr Thr Lys Gly Leu Leu Trp Arg Arg	
305 310	
act tga tga gag ggt att cat caa tga aga gga tag ctt act tgg atc	3116
Thr Glu Gly Ile His Gln Arg Gly Leu Thr Trp Ile	
315 320 325	
tgg aag ctt atc tgc agg agc tgt taa tat tac tgg tgt taa gag gaa	3164
Trp Lys Leu Ile Cys Arg Ser Cys Tyr Tyr Trp Cys Glu Glu	
330 335	
aat tga tgc ttt gag ctc acc tgc aag gac att tat aag ccc act ttc	3212
Asn Cys Phe Glu Leu Thr Cys Lys Asp Ile Tyr Lys Pro Thr Phe	
340 345 350	
tcc tca taa gtc gcc tgc tgc taa gac aaa tgg tat tag cgg tgc tac	3260
Ser Ser Val Ala Cys Cys Asp Lys Trp Tyr Arg Cys Tyr	
355 360 365	
caa gtt ggc agc aac acc agt gag cac agc aat gac aac tgc caa gtg	3308
Gln Val Gly Ser Asn Thr Ser Glu His Ser Asn Asp Asn Cys Gln Val	
370 375 380	
gct cag gac tgt cat atc ccc gct tct gcc aaa acc ttc tcc tgg gtt	3356
Ala Gln Asp Cys His Ile Pro Ala Ser Ala Lys Thr Phe Ser Trp Val	
385 390 395	
gga aca ttt cct taa atc atg tga tag gga tat aac aaa tga cgt cac	3404
Gly Thr Phe Pro Ile Met Gly Tyr Asn Lys Arg His	
400 405 410	
acg aag agc aca cat aat att gga agc tat ttt ccc aaa tag ttc cct	3452
Thr Lys Ser Thr His Asn Ile Gly Ser Tyr Phe Pro Lys Phe Pro	
415 420 425	
tgg tgc cca atg tgg agg tgg aag ttt gca agc tgt tga cct gat gga	3500
Trp Cys Pro Met Trp Arg Trp Lys Phe Ala Ser Cys Pro Asp Gly	
430 435 440	
tga cat atg ggc aga gca gcg cag att aga agc ttg taa gtt ata cta	3548
His Met Gly Arg Ala Ala Gln Ile Arg Ser Leu Val Ile Leu	
445 450 455	
cag agt tct tga ggc aat gtg taa agc aga agc tca gat ttt gca tgc	3596

sequence listing S-92981.ST25

Gln Ser Ser	Gly Asn Val	Ser Arg Ser Ser Asp Phe Ala Cys	
	460	465	
aaa taa tct gaa ctc ttt att gac aaa tga gag gtt cca tag atg cat			3644
Lys Ser Glu Leu Phe Ile Asp Lys Glu Val Pro Met His	470	475 480	
gct tgc ttg ctc agc tga att ggt act ggc tac cca caa aac aat tac			3692
Ala Cys Leu Leu Ser Ile Gly Thr Gly Tyr Pro Gln Asn Asn Tyr	485	490 495	
aat gtt gtt ccc agc tgt tct gga gag gac tgg gat cac agc ctt tga			3740
Asn Val Val Pro Ser Cys Ser Gly Glu Asp Trp Asp His Ser Leu	500	505 510	
tct cag caa ggt aat tga gag ttt cat acg aca tga aga ttc tct gcc			3788
Ser Gln Gln Gly Asn Glu Phe His Thr Thr Arg Phe Ser Ala	515	520 525	
tag aga gtt gag acg aca tct gaa ttc act gga gga acg gct tct aga			3836
Arg Val Glu Thr Thr Ser Glu Phe Thr Gly Gly Thr Ala Ser Arg	530	535 540	
gag tat ggt atg gga gaa agg ctc ttc aat gta caa ttc tct gat tgt			3884
Glu Tyr Gly Met Gly Glu Arg Leu Phe Asn Val Gln Phe Ser Asp Cys	545	550 555	
tgc cag gcc atc gct tgc att gga gat aaa tca gct cgg ttt act agc			3932
Cys Gln Ala Ile Ala Cys Ile Gly Asp Lys Ser Ala Arg Phe Thr Ser	560	565 570	
tga acc aat gcc atc tct gga tgc aat cgc agc act tat taa ttt ctc			3980
Thr Asn Ala Ile Ser Gly Cys Asn Arg Ser Thr Tyr Phe Leu	575	580 585	
tga cgg agc aaa tca tgc atc atc tgt aca aaa gca tga aac ttg tcc a			4029
Arg Ser Lys Ser Cys Ile Ile Cys Thr Lys Ala Asn Leu Ser	590	595 600	
ggtagtttta tttgtttctg aattaaagca gttttccaac ctgctgttaa tggtatgatt			4089
ttcttaccaa aaattgtcaa atttgctgcc atata gg aca aaa tgg ggg gat			4141
		Arg Thr Lys Trp Gly Asp	605
tag atc gcc caa aag att atg tac tga tta ccg cag cat tct agt tga			4189
Ile Ala Gln Lys Ile Met Tyr Leu Pro Gln His Ser Ser	610	615 620	
acg caa ttc ctt tac atc acc agt aaa gga tgc tct gtt ggc ctt agg			4237
Thr Gln Phe Leu Tyr Ile Thr Ser Lys Gly Ser Ser Val Gly Leu Arg	625	630 635	
caa cgt taa atc caa gat gct gcc acc tcc gtt gca gtc tgc att tgc			4285
Gln Arg Ile Gln Asp Ala Ala Thr Ser Val Ala Val Cys Ile Cys	640	645 650	
ca ggtacatttt gagtaactat gagtagaaat ggagagtttag tttacctatc			4337
Gln			

sequence listing S-92981.ST25

tagttgtccc tgtacttggt aagtaacctc ttcggattta tgtctaca g ccc aac Pro Asn	4392
acg gcc caa ccc agg agg tgg agg aga aac ttg tgc aga aac tgg aat Thr Ala Gln Pro Arg Arg Trp Arg Arg Asn Leu Cys Arg Asn Trp Asn 655 660 665 670	4440
caa tat ttt ctt cac aaa ggtaggtctg tgagatcttt ggatctacta Gln Tyr Phe Leu His Lys 675	4488
ctaatacgttt ggtagatga tgtactacaa aacacggtat tgattcttca ttttcggctg	4548
ggaattgtgt taaatgtggt ggctcttccc a gat taa taa att ggc tgc tgt Asp Ile Gly Cys Cys 680	4600
aag aat caa tgg aat ggt gga aag act aca act ttc aca gca aat aag Lys Asn Gln Trp Asn Gly Gly Lys Thr Thr Thr Phe Thr Ala Asn Lys 685 690 695	4648
gga gag tgt gta ttg ttt ctt cca aca tgt act tgc tca gcg gac ttc Gly Glu Cys Val Leu Phe Leu Pro Thr Cys Thr Cys Ser Ala Asp Phe 700 705 710	4696
tct ttt att cag tgc aca cat tga cca gat cat tct ctg ttg ctt cta Ser Phe Ile Gln Ser Thr His Pro Asp His Ser Leu Leu Leu Leu 715 720 725	4744
cgg agt ggc caa ggtgagtagt gtgattcaaa gggtttaact atatgtcatc Arg Ser Gly Gln 730	4796
tggtttacaa tggcttctct tacacttaca ctttttccat gaatcacctt gtagatatcc	4856
caaagagacc tga ctt tca ggg aaa tca tat aca act acc gga agc aac Leu Ser Gly Lys Ser Tyr Thr Thr Thr Gly Ser Asn 735 740	4905
cac agt gta aac cat tag ttt tcc gca gcg ttt atg tgg atg cgt tac His Ser Val Asn His Phe Ser Ala Ala Phe Met Trp Met Arg Tyr 745 750 755	4953
aat gtc gcc gtc aag g ggtatatata cactottaac cttatgctga aaagtttctt Asn Val Ala Val Lys 760	5009
tactcgggtgg agaagactaa atttgtgaca atgacttgaa ca ga gaa tag ggc Gly Glu Gly	5062
cag atc atg ttg aca tca tca cat tct aca atg aaa tat tta ttc ctg Gln Ile Met Leu Thr Ser Ser His Ser Thr Met Lys Tyr Leu Phe Leu 770 775 780	5110
ccg taa agc cgc tgc tgg tgg agc tag gtc ctg taa gaa acg acc ggg	5158

sequence listing S-92981.ST25

Pro	Ser	Arg	Cys	Trp	Trp	Ser	Val	Leu	Glu	Thr	Thr	Gly	
	785					790						795	
ctg tgg aag cca ata ata agc ctg aa						ggtagttaag		aaaggccaga					5204
Leu Trp Lys Pro Ile Ile Ser Leu Lys													
	800												
tacttgtag atgtaagctt tgtctatcaa tttagtcctt aagttaaatg atcgtcttat													5264
tttggattca ca g gtc aat gtc ccg gat cgc caa agg tgt ctg tgt ttc													5313
		Val	Asn	Val	Pro	Asp	Arg	Gln	Arg	Cys	Leu	Cys	Phe
						810					815		
caa gtg ttc cag aca tgt ccc cta aaa aag tat ctg cag tgc aca atg													5361
Gln Val Phe Gln Thr Cys Pro Leu Lys Lys Tyr Leu Gln Cys Thr Met													
	820					825					830		
ttt atg ttt ctc ctc ttc ggg gat caa ag gtaaagaaga tcatagtgt													5410
Phe Met Phe Leu Leu Phe Gly Asp Gln Arg													
	835					840							
taactcttta tcatgatatg actaagtctt gaggaggagg taggtgacaa gattgtttgg													5470
ttaccttcca tgtgttgtgt gtttgca g atg gat gct ctt att tca cac agt													5522
						Met	Asp	Ala	Leu	Ile	Ser	His	Ser
							845					850	
aca aag agt tac tat gct tgt gtt gga gag agt aca cat gct tac cag													5570
Thr Lys Ser Tyr Tyr Ala Cys Val Gly Glu Ser Thr His Ala Tyr Gln													
	855					860						865	
agc cct tca aag gac cta tct gcc atc aac aac cgc ttg aac a													5613
Ser Pro Ser Lys Asp Leu Ser Ala Ile Asn Asn Arg Leu Asn													
	870					875						880	
agtaagtaaa aaaatcacgt ctctcatcag cttcttccat aaaaccaatc actgacccaa													5673
tccaatttca tctggtgtca ca gc agc agc agc aac cgc aag agg acg cta													5724
						Ser	Ser	Ser	Ser	Asn	Arg	Lys	Arg
													890
						885							
aac ttt gac gca gaa gca ggg atg gtc agc gat tcc atg gta gca aat													5772
Asn Phe Asp Ala Glu Ala Gly Met Val Ser Asp Ser Met Val Ala Asn													
	895					900						905	
agc ctt aac ctc caa aac caa aat caa aac caa aat gga agc gat gca													5820
Ser Leu Asn Leu Gln Asn Gln Asn Gln Asn Gln Asn Gly Ser Asp Ala													
	910					915						920	
tcg tcc tca ggt ggt gcc gca ccc ctt aaa acc gag cca aca gat tca													5868
Ser Ser Ser Gly Gly Ala Ala Pro Leu Lys Thr Glu Pro Thr Asp Ser													
	925					930						935	
ta gatattcttc totacttgct acaccaactt ctcttcagtt atagcatctg													5920
taaatcctta tgttgagag tttgctttta tgtttagctt tctagtttat agtgatcacc													5980
tcaggctatg agcggatgga tccctttatt gtttcttttt tcttttttta tcttagttaa													6040

sequence listing S-92981.ST25

gtcagtcotta ataagcatta ataaatgtct ttttcttggt cactctttct aactgtgttc	6100
ggtgtcccat ctactaaatt tattttccac tttaaaaaaa aacaatttgt gacatttact	6160
taacttgga catatacagt acagttaagc aattaactat aaccaacaaa ttgtctgaac	6220
aattgtctgt cttacctttt tagctctcta taaatttacg ccgcaaaaca acactttatg	6280
tcgatttcag aataacttac tactccagca tatttctcaa aactttctca atagggtaaa	6340
tttaaaacaa ctttgcaact tatgaaaaaa tcctccagca aatttgccag aaaagaatgt	6400
tacaatggct acaatcacat cc	6422